Kindly replace the paragraph beginning at page 13, line 13, with the following:

B2 --Cloning of cDNA - A degenerate primer (SEQ ID NO.:5)--

Kindly replace the paragraph beginning at page 14, line 4, with the following:

--Probes were generated from total RNAs isolated from developing seeds of the glanded and glandless *G. hirsutum* cultivars, respectively, and the first strand cDNA was synthesized as previously described (Meng et al (1999) *J. Nat. Prod.* **62**, 248-252). The cDNAs were ^{32}P-labeled using a random DNA labeling kit (Takara, Dalian, China), and used for dot-hybridizations. Clones *LP132* and *LP64* showing preferential hybridization with probes of glanded seeds were selected and sequenced by the dideoxynucleotide chain termination method. Specific primers LP132F (SEQ ID NO.:7) [5¢-TGACTGATCATGAGAAGCT (sense)] and LP132R (SEQ ID NO.:8) [5¢-GTGCTGGAGATTTGATGGT (reverse)] based on the sequence of *LP132* were then used for screening the *G. arboreum* cDNA library by using a PCR 96-well plate method (Liu et al (1999) *Mol. Plant Microbe Interact.* **12**, 1095-1104). A cDNA clone, *CYP706B1*, was then isolated and sequenced (See SEQ. ID. NO. 1; GenBank/EBI Data Bank Accession No. AF332974).--

B3

Kindly replace the paragraph beginning at page 15, line 3, with the following:

--Pericarp (approx. 3 mm thick) was peeled from bolls with a blade. Total RNAs were isolated from tissues or from suspension cultured cells by a cold phenol method, and

B4

the transcripts were analyzed by RT-PCR with primers LP132F and LP132R for *CYP706B1* (position 1433 ~ 1689), 97400 (SEQ ID NO.:9) [5¢-CACATCC(AC)TTCGATTCCGAC (sense)] and 97T580 (SEQ ID NO.:10) [5¢-AGGCTTAAATGGTGGGTGGT (reverse)] for *CAD1-C* (position 398 ~ 610), and H3F (SEQ ID NO.:11) [5¢-GAAGCCTCATCGATACCGTC (sense)] and H3R (SEQ ID NO.:12) [5¢-CTACCACTACCATCATGTC (reverse)] for the histone gene *his3* (positions 95 ~ 526). For Northern analysis, 10 mg of RNA per lane were separated by electrophoresis, blotted onto a nitrocellulose membrane, and the blots were hybridized with ^{32}P labeled DNA probes of either *CYP706B1* (see above) or *CAD1-C1* (Liu et al (1999) *Mol. Plant Microbe Interact.* **12**, 1095-1104). After hybridization and washing, the blots were exposed to X-ray film for 2 days.

Kindly replace the paragraph beginning on page 15, line 14 with the following:

Expression in yeast cells and enzyme assay - The yeast *Saccharomyces cerevisiae* strain W(R), which overexpresses the yeast cytochrome P450 reductase when grow on galactose, and the expression vector pYeDP60 were provided by D. Pompon (Pompon et al (1996) *Methods Enzymol.* **272**, 51-64). The cDNA of CYP706B1 was modified by PCR with a 5'-terminal primer (SEQ ID NO.:13) 5¢-GGGTACCATGTTGCAAATAGCTTTCAG (sense), in which a *Kpn* I site was introduced, and a 3'-terminal primer (SEQ ID NO.:14) 5¢-GGGAGCTCTTACTTCATATAGTGCTGGA (reverse), in which a *Sac* I site was introduced. PCR was conducted on plasmid DNA by using

Pyrobest™ DNA polymerase (TaKaRa). After digestion with the restriction enzymes, the fragment was inserted into pYeDP60. Plasmid DNA was introduced into yeast cells by a LiAc method, transformed yeast cells were then selected, cultured, and induced, and microsomes were prepared following a high density procedure (Pompon et al (1996) *Methods Enzymol.* **272**, 51-64).

Kindly replace the paragraph beginning on page 19, line 20 with the following:

-- Sequence analysis revealed several structural motifs characteristic of eukaryotic P450s (Fig. 2). The highly conserved heme-binding motif FxxGxRxCxG (Chapple, C. (1998) *Ann. Rev. Plant Physiol. Plant Mol. Biol.* 49, 311-343) was found in CYP706B1 (SEQ ID NO.:15) as FGSGRRMCAG, 73 amino acid residues from the C-terminus. In most plant P450s, there is a proline residue immediately after the invariant heme-binding cysteine (Schalk et al (1999) *Biochemistry* 38, 6093-61103); however, in CYP706B1, this proline is replaced by alanine. The proline-rich region immediately after the N-terminal signal anchor sequence (Nelson, D. R., and Strobel, H. W. (1988) *J. Biol. Chem.* 263, 6038-6050), with a consensus of (SEQ ID NO.:16) (P/I)PGPx(G/P)xP (Schalk et al (1999) *Biochemistry* 38, 6093-61103), was completely conserved in this cotton P450 as PPGPRGLP (SEQ ID NO.: 17). In addition, the threonine-containing pocket for binding an oxygen molecule, with a consensus of (SEQ ID NO.:18) (A/G)Gx(D/E)T(T/S) (Durst, F., and Nelson, D. R. (1995) *Drug Metab. Drug Interact.* 12, 189-206), was also found (as GGTDTT) (SEQ ID NO.:19). --

In compliance with 37 C.F.R. § 1.823(a), please substitute the attached paper copy of the Sequence Listing for the Sequence Listing originally filed with the application on pages 29-31 of the specification. Please renumber the pages accordingly.

REMARKS

Entry of the foregoing and favorable consideration of the subject application, in light of the following remarks, are respectfully requested.

By the foregoing amendment, the specification has been amended to replace the originally filed Sequence Listing with a substitute Sequence Listing and to include the sequence identifiers at the appropriate locations throughout the specification.

In the event that there are any questions relating to this Preliminary Amendment, or the application in general, it would be appreciated if the Examiner would telephone the undersigned attorney concerning such questions so that prosecution of this application may be expedited.

Respectfully submitted,

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